

# Yong-Joon Cho

## List of Publications by Year in Descending Order

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**Version:** 2024-04-09

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

60 papers	5,431 citations	18 h-index	62 g-index
62 ext. papers	5,957 ext. citations	4.2 avg, IF	5.06 L-index

#	Paper	IF	Citations
60	Regulation of iron homeostasis by peroxide-sensitive CatR, a Fur-family regulator in <i>Streptomyces coelicolor</i> . <i>Journal of Microbiology</i> , <b>2021</b> , 59, 1083-1091	3	
59	Functional dissection of the phosphotransferase system provides insight into the prevalence of <i>Faecalibacterium prausnitzii</i> in the host intestinal environment. <i>Environmental Microbiology</i> , <b>2021</b> , 23, 4726-4740	5.2	3
58	Draft Genome Sequence of the Chitin-Degrading Psychrotolerant Bacterium <i>Pedobacter jejuensis</i> TN23, Isolated from Antarctic Soil. <i>Microbiology Resource Announcements</i> , <b>2021</b> , 10, e0052321	1.3	
57	A large-scale metagenomic study for enzyme profiles using the focused identification of the NGS-based definitive enzyme research (FINDER) strategy. <i>Biotechnology and Bioengineering</i> , <b>2021</b> , 118, 4360-4374	4.9	1
56	Genomic Multiplication and Drug Efflux Influence Ketoconazole Resistance in. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2020</b> , 10, 191	5.9	5
55	A Transcriptional Regulatory Map of Iron Homeostasis Reveals a New Control Circuit for Capsule Formation in. <i>Genetics</i> , <b>2020</b> , 215, 1171-1189	4	3
54	Microbial Diversity in Moonmilk of Baeg-nyong Cave, Korean CZO. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 613	5.7	7
53	gen. nov., sp. nov., a member of the family isolated from an Antarctic lichen. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2020</b> , 70, 5918-5925	2.2	2
52	The role of Rsv1 in the transcriptional regulation of genes involved in sugar metabolism for long-term survival. <i>FEBS Journal</i> , <b>2020</b> , 287, 878-896	5.7	5
51	A Novel Virus Alters Gene Expression and Vacuolar Morphology in Cells and Induces a TLR3-Mediated Inflammatory Immune Response. <i>MBio</i> , <b>2020</b> , 11,	7.8	5
50	Methane production in the oxygenated water column of a perennially ice-covered Antarctic lake. <i>Limnology and Oceanography</i> , <b>2020</b> , 65, 143-156	4.8	6
49	Resequencing the Genome of Strain KCTC 27527. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	6
48	Draft Genome Sequence of <i>Arthrobacter oryzae</i> TNBS02, a Bacterium Containing Heavy Metal Resistance Genes, Isolated from Soil of Antarctica. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	1
47	Antifungal Mechanism of Action of Lauryl Betaine Against Skin-Associated Fungus. <i>Mycobiology</i> , <b>2019</b> , 47, 242-249	1.7	5
46	The <i>Salmonella</i> virulence protein MgtC promotes phosphate uptake inside macrophages. <i>Nature Communications</i> , <b>2019</b> , 10, 3326	17.4	13
45	Microbial diversity of Baeg-nyong cave and characterization of the antibiotics extracted from <i>Streptomyces exfoliatus</i> . <i>FASEB Journal</i> , <b>2019</b> , 33, 637.4	0.9	1
44	The latitudinal gradient in rock-inhabiting bacterial community compositions in Victoria Land, Antarctica. <i>Science of the Total Environment</i> , <b>2019</b> , 657, 731-738	10.2	6

43	Understanding the Mechanism of Action of the Anti-Dandruff Agent Zinc Pyrithione against <i>Malassezia restricta</i> . <i>Scientific Reports</i> , <b>2018</b> , 8, 12086	4.9	23
42	Genomic Tandem Quadruplication is Associated with Ketoconazole Resistance in. <i>Journal of Microbiology and Biotechnology</i> , <b>2018</b> , 28, 1937-1945	3.3	16
41	Whole genome sequencing analysis of the cutaneous pathogenic yeast <i>Malassezia restricta</i> and identification of the major lipase expressed on the scalp of patients with dandruff. <i>Mycoses</i> , <b>2017</b> , 60, 188-197	5.2	34
40	Complete genome sequence of <i>Pseudomonas antarctica</i> PAMC 27494, a bacteriocin-producing psychrophile isolated from Antarctica. <i>Journal of Biotechnology</i> , <b>2017</b> , 259, 15-18	3.7	13
39	sp. nov., isolated from stream water. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2017</b> , 67, 153-157	2.2	6
38	Synonymy of and and Emended Description of. <i>Journal of Microbiology and Biotechnology</i> , <b>2017</b> , 27, 149-154	3.54	1
37	Time-resolved pathogenic gene expression analysis of the plant pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>BMC Genomics</i> , <b>2016</b> , 17, 345	4.5	19
36	Draft genome sequence of the extremely halophilic archaeon <i>Haladaptatus cibarius</i> type strain D43(T) isolated from fermented seafood. <i>Standards in Genomic Sciences</i> , <b>2015</b> , 10, 53		3
35	Reclassification of <i>Serpens flexibilis</i> Hespell 1977 as <i>Pseudomonas flexibilis</i> comb. nov., with <i>Pseudomonas tuomuerensis</i> Xin et al. 2009 as a later heterotypic synonym. <i>Systematic and Applied Microbiology</i> , <b>2015</b> , 38, 563-6	4.2	7
34	Genome sequence of the haloarchaeon <i>Haloterrigena jeotgali</i> type strain A29(T) isolated from salt-fermented food. <i>Standards in Genomic Sciences</i> , <b>2015</b> , 10, 49		4
33	Complete Genome Sequence of Middle East Respiratory Syndrome Coronavirus KOR/KNIH/002_05_2015, Isolated in South Korea. <i>Genome Announcements</i> , <b>2015</b> , 3,		35
32	EzEditor: a versatile sequence alignment editor for both rRNA- and protein-coding genes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2014</b> , 64, 689-691	2.2	109
31	Non-contiguous finished genome sequence and description of the gliding bacterium <i>Flavobacterium seoulense</i> sp. nov. <i>Standards in Genomic Sciences</i> , <b>2014</b> , 9, 34		5
30	A vanillin derivative causes mitochondrial dysfunction and triggers oxidative stress in <i>Cryptococcus neoformans</i> . <i>PLoS ONE</i> , <b>2014</b> , 9, e89122	3.7	32
29	Profiling bacterial community in upper respiratory tracts. <i>BMC Infectious Diseases</i> , <b>2014</b> , 14, 583	4	48
28	Draft Genome Sequence of <i>Kitasatospora cheerisanensis</i> KCTC 2395, Which Produces Plecomacrolide against Phytopathogenic Fungi. <i>Genome Announcements</i> , <b>2014</b> , 2,		5
27	Complete genome sequence of <i>Hymenobacter swuensis</i> , an ionizing-radiation resistant bacterium isolated from mountain soil. <i>Journal of Biotechnology</i> , <b>2014</b> , 178, 65-6	3.7	9
26	Genome sequence of the chromate-resistant bacterium <i>Leucobacter salsicium</i> type strain M1-8(T). <i>Standards in Genomic Sciences</i> , <b>2014</b> , 9, 495-504		7

25	Draft genome sequence of <i>Pseudomonas</i> sp. strain G5, isolated from a traditional indigo fermentation dye vat <b>2013</b> , 56, 339-341		1
24	Functional screening of a metagenomic library reveals operons responsible for enhanced intestinal colonization by gut commensal microbes. <i>Applied and Environmental Microbiology</i> , <b>2013</b> , 79, 3829-38	4.8	20
23	<i>Fretibacter rubidus</i> gen. nov., sp. nov., isolated from seawater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2013</b> , 63, 4633-4638	2.2	7
22	Genome sequence of the moderately halophilic bacterium <i>Salinicoccus carniancri</i> type strain Crm(T) (= DSM 23852(T)). <i>Standards in Genomic Sciences</i> , <b>2013</b> , 8, 255-63		6
21	The genome sequence of <i>Mycobacterium massiliense</i> strain CIP 108297 suggests the independent taxonomic status of the <i>Mycobacterium abscessus</i> complex at the subspecies level. <i>PLoS ONE</i> , <b>2013</b> , 8, e81560	3.7	44
20	Transcriptomic analysis of genes modulated by cyclo(L-phenylalanine-L-proline) in <i>Vibrio vulnificus</i> . <i>Journal of Microbiology and Biotechnology</i> , <b>2013</b> , 23, 1791-801	3.3	10
19	Draft Genome sequence of <i>Escherichia coli</i> AI27, a porcine isolate belonging to phylogenetic group B1. <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 6640-1	3.5	1
18	A defect in iron uptake enhances the susceptibility of <i>Cryptococcus neoformans</i> to azole antifungal drugs. <i>Fungal Genetics and Biology</i> , <b>2012</b> , 49, 955-66	3.9	41
17	Introducing EzTaxon-e: a prokaryotic 16S rRNA gene sequence database with phylotypes that represent uncultured species. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2012</b> , 62, 716-721	2.2	4480
16	Comparative genomics of <i>Neisseria weaveri</i> clarifies the taxonomy of this species and identifies genetic determinants that may be associated with virulence. <i>FEMS Microbiology Letters</i> , <b>2012</b> , 328, 100-5	2.9	11
15	Genome sequence of <i>Escherichia coli</i> J53, a reference strain for genetic studies. <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 3742-3	3.5	36
14	Draft genome sequence of <i>Escherichia coli</i> W26, an enteric strain isolated from cow feces. <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 5149-50	3.5	4
13	Draft genome sequence of <i>Mycobacterium abscessus</i> subsp. <i>bolletii</i> BD(T). <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 2756-7	3.5	27
12	Toll-like receptor 9 mediates oral bacteria-induced IL-8 expression in gingival epithelial cells. <i>Immunology and Cell Biology</i> , <b>2012</b> , 90, 655-63	5	16
11	Genome sequence of <i>Lactobacillus ruminis</i> SPM0211, isolated from a fecal sample from a healthy Korean. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 5034	3.5	5
10	Genome sequence of <i>Escherichia coli</i> AA86, isolated from cow feces. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 3681	3.5	7
9	Draft genome sequence of <i>Shewanella</i> sp. strain HN-41, which produces arsenic-sulfide nanotubes. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 5039-40	3.5	3
8	Complete genome sequence of <i>Vibrio vulnificus</i> MO6-24/O. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 2062-3	3.5	55

7	Genome sequence of <i>Lactobacillus salivarius</i> GJ-24, a probiotic strain isolated from healthy adult intestine. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 5021-2	3.5	12
6	Duplex-specific nuclease efficiently removes rRNA for prokaryotic RNA-seq. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, e140	20.1	93
5	Complete genome sequence analysis of <i>Leuconostoc kimchii</i> IMSNU 11154. <i>Journal of Bacteriology</i> , <b>2010</b> , 192, 3844-5	3.5	23
4	Genomic evolution of <i>Vibrio cholerae</i> . <i>Current Opinion in Microbiology</i> , <b>2010</b> , 13, 646-51	7.9	39
3	Synthesis of gamma-glutamylcysteine as a major low-molecular-weight thiol in lactic acid bacteria <i>Leuconostoc</i> spp. <i>Biochemical and Biophysical Research Communications</i> , <b>2008</b> , 369, 1047-51	3.4	28
2	Differential expression and role of two dithiol glutaredoxins Grx1 and Grx2 in <i>Schizosaccharomyces pombe</i> . <i>Biochemical and Biophysical Research Communications</i> , <b>2004</b> , 321, 922-9	3.4	15
1	A novel virus alters gene expression and vacuolar morphology in <i>Malassezia</i> cells and induces a TLR3-mediated inflammatory immune response		2